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(54) Method for the rapid determination of bacteria

(57) The invention relates to the detection, identification and diagnosis of bacteria in samples in general and in particular in clinical samples such as blood, urine, saliva, cerebrospinal fluid that are taken from patients that are possibly infected with a, as yet unknown, possibly pathogenic bacterium, or during follow-up diagnostic testing to for example evaluate therapeutic measures that have been taken so far to treat the disease.

The invention provides a method for detecting or identifying a bacterium suspected of being present in a sample comprising testing said sample by Gram-staining and testing said sample with a probe according to an *in situ* hybridisation protocol selected on the basis of the outcome of said Gram-staining. The invention also provides probes for use in said method.

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Description

[0001] The invention relates to the detection, identification or determination of bacteria in samples in general and in particular in clinical samples such as blood, urine, saliva, cerebrospinal fluid, faeces, pus and tissue that are taken from patients that are possibly infected with a, as yet unknown, possibly pathogenic bacterium, or during follow-up diagnostic testing to for example evaluate therapeutic measures that have been taken so far to treat the disease.

[0002] Traditional methods to determine or identify bacteria in general start with a Gram-stain, which is well known in the art. Such a stain can be performed on a sample immediately after sampling or, when not enough bacteria are present, after a short period of culturing of the sample. In general, four types of bacteria are found after Gram-staining; Gram-negative rods and cocci and Gram-positive rods and cocci. However, such a Gram-stain can only in very exceptional cases provide the clinician with the knowledge required to provide accurate therapy.

[0003] Examples of Gram-negative rods in clinical samples are *Enterobacter*, *Klebsiella*, *Salmonella*, *Escherichia*, *Proteus* and *Pseudomonas species*, of Gram-negative cocci are *Neisseria species*. Gram-positive rods that may be found in clinical samples are *Bacillus species*, of Gram-positive cocci are *Enterococcus*, *Streptococcus* and *Staphylococcus species*. Some of these, such as *Streptococcus* and *Staphylococcus* can easily be further determined or distinguished from each other by their morphological characteristics. *Streptococci* (and *Enterococci*) are characterised by chain-like character of cocci that are linked to each other whereas *Staphylococci* accumulate in clumps. Most other species, such as *Enterococcus* and *Streptococcus species* cannot be distinguished by morphology alone. However, such relatively rough taxonomic distinction on a genus level cannot be considered satisfactory for clinical purposes and consequently further identification is required to establish proper medication. For example in the case of *Staphylococcus*, these bacteria need to be further distinguished based on their coagulase positive (*S. aureus*) or coagulase negative (*S. haemolyticus* and others) character because these two groups require different antibiotic therapy.

[0004] In general, the exact species involved is determined by culturing techniques. To fully determine the species of a bacterium present in a clinical sample the following steps are in general required;

- (1) Pre-culturing of the sample in order to amplify the number of bacteria to a level above the lower detection limits of step (2).
- (2) Culturing on selective and non-selective media.

[0005] These traditional methods are time consuming. On average, a regular diagnostic procedure takes at least a few hours (minimally 2) of pre-culturing followed by minimally 24 hours of culturing on selective and non-selective media. This implies that it takes at least 26 hours before the clinician obtains a diagnosis on which he or she can select appropriate antibiotics or base other further treatment.

[0006] This latency-period between the sampling of a patient and the final diagnosis in most cases is critical for the treatment and the speed-of-recovery of the patient. During this latency-period a patient is in general treated with broad-spectrum antibiotics. The antibiotic of choice is mainly determined by the "clinical eye" of the clinician.

[0007] By selecting a broad-spectrum antibiotic, such therapies are in general successful in the eradication of the pathogen but a serious side effect of this strategy is the fact that in most instances the normal microbial flora is affected also. This side-effect heavily decreases the patients defence against microbial invaders from the environment. Especially the lowering of the colonisation threshold of the gastro-intestinal tract may cause severe overgrowth by e.g. yeasts and fungi. The resulting secondary infection, or super-infection, in septicaemic patients who already suffer from a decreased immunity often leads to life-threatening situations.

[0008] Apart from the serious danger to the patient's health, wide-spectrum antibiotic therapy poses another threat. The repeated exposure of indigenous bacteria to antibiotics enhances the emergence of resistance against such an antibiotic. Especially when a resistance-gene is encoded on a plasmid, other (potential pathogenic) bacterial species may become resistant after the uptake of the plasmid. This latter scenario is considered to be a major problem in hospital epidemiology. It is therefore of paramount therapeutic and epidemiological importance to speed up the methodological procedures in the diagnosis of blood samples from for example septicaemic patients to be able to select specific antibiotic therapy designed for the specific pathogen found, thereby refraining from using broad-spectrum antibiotics.

[0009] Also, in those cases where resistance of a pathogen to antibiotics has already occurred, it is of utmost importance to be able to rapidly identify the pathogen and rapidly select the antibiotic against which the pathogen is not resistant.

[0010] In short, there is a need for fast and reliable diagnosis of bacteria, present in for example clinical samples that may replace or add to the currently used culturing techniques. Present techniques other than culturing, albeit in general specific when beforehand knowledge exists about the species involved, cannot be used with samples containing uncharacterised species or are too slow to meet the needs of the clinician in providing care to his or her patients.

[0011] The invention provides a method for determining, detecting or identifying a bacterium suspected of being present in a sample comprising

a) testing said sample by Gram-staining and

b) testing said sample with a probe according to an *in situ* hybridisation protocol selected on the basis of the outcome of said Gram-staining.

[0012] Rapid techniques for detecting bacteria and other bacteria in general are known. For example, *in situ* hybridisation is a well known technique, however, in general it has only been applied in specialised laboratories as a tool to detect and quantify the relative abundance of bacteria that are difficult to culture using traditional methodology or as a tool to quantify for example growth kinetics of already known bacteria in culture.

[0013] In short, in *in situ* hybridisation, nucleic acid probes, labelled with a reporter molecule such as an enzyme or a fluorescing substance, are reacted with specific nucleic acid sequences found specifically and preferably solely in the bacteria under study, which for this purpose has been permeabilised to let the probe enter the organism. As a target sequence nucleic acids of different origins are employed. Most commonly used as a target for *in situ* hybridisation is the 16S ribosomal RNA molecule. Other target molecules which can be used are: 23S ribosomal RNA, mitochondrial RNA, messenger RNA and nuclear DNA.

[0014] *In situ* hybridisation has never been successfully applied for rapid detection of bacteria in clinical samples because the presently used *in situ* hybridisation techniques are too inaccurate and too slow to give an advantage over traditional culturing.

[0015] First of all, hybridisation requires permeabilisation of the pathogen, and until now no generally applicable permeabilisation protocols have been developed that allow sufficient but restricted lysis of many or all of a broad range of unidentified bacteria. In general, mild permeabilisation leaves many bacteria (such as *Staphylococcus spec.*) inaccessible for subsequent hybridisation with probes, whereas rigorous permeabilisation often fully lyses most bacteria, thereby foregoing the possibility to detect them all together.

[0016] In addition, current protocols are in general time-consuming multi-step procedures; hybridisation often requires minimally 24 hours, thereby giving no relief to the needs of the clinician who is only helped with accurate and speedy diagnosis. Furthermore, they mostly require beforehand knowledge about the genus or even species involved in order to select appropriate probes; having such beforehand knowledge is clearly not the case in the event of a patient having an unidentified infection. Also, the present, already inappropriate hybridisation techniques do not allow to gather information on the response against antibiotics of the bacterium involved.

[0017] The invention provides a fast and reliable method for diagnosis, detection and/or determination of bacteria which may be present in a sample. Such a sample may be of various origin, it is for instance possible to apply a method as provided by the invention to a sample obtained from a (contaminated) bacterial culture, or drinking water or food suspected to be contaminated with a bacterium.

[0018] In a preferred embodiment the invention provides a method to detect or identify a bacterium suspected of being present in a clinical sample. Herein, the term "clinical sample" comprises a sample obtained or derived from an animal, preferably a mammal, more preferably a human being. Such a sample may be sampled or tested because a bacterial infection or disease is suspected. Such a sample can be of various origin, such as blood, serum, white blood cells, cerebrospinal fluid, synovial fluid, tissue, biopsies, urine, saliva, faeces, and others. In a preferred embodiment the invention provides a method wherein said sample is mammalian blood, preferably being derived from a human.

[0019] A sample can be a primary sample or it can be a secondary or sub-sample which is derived from a primary sample by diluting, splitting or culturing it one or more times. Diluting allows determining the relative abundance of a bacterium in a sample, thereby thus providing a method allowing not only qualitative but also quantitative determination of a bacterium. A sample can be tested directly after it has been obtained or after it has been stored, for example by cooling or freezing and secondary or sub-samples can be tested in parallel or subsequent from each other.

[0020] The invention provides a method comprising determining by Gram-staining the Gram-positive or Gram-negative and rod or coccus type of bacterium in a clinical sample and further testing said sample according to an *in situ* hybridisation protocol selected on the basis of the outcome of said Gram-staining.

[0021] A preferred embodiment of the invention is a method for the detection or identification of bacteria in a clinical sample of blood of patients who are suspected to suffer from a septicaemia. In a preferred embodiment a method provided by the invention makes use of labeled probes, such as fluorescently labeled single strain DNA-, RNA- or PNA-probes, directed against specific target sequences on for example the ribosomal RNA of the target bacterium present in the sample.

[0022] The invention provides a method wherein classical Gram-staining indicates the presence of a Gram-negative or Gram-positive bacterium in said sample, further comprising determining the rod or coccus character of said bacterium, thereby establishing the subsequent testing protocol.

[0023] When a Gram-negative bacterium is of the rod type, the invention provides a method further comprising hybridising said sample with at least one probe selected from a group of probes capable of hybridising with nucleic acid found in *Escherichia coli*, in *Klebsiella pneumoniae*, in *Klebsiella oxytoca*, in *Serratia marcescens*, in *Enterobacter aerogenes*, in *Enterobacter cloacae*, in *Proteus vulgaris*, in *Proteus mirabilis*, in *Salmonella typhi*, in *Pseudomonas*

aeruginosa.

[0024] Furthermore, the invention provides a method wherein said character is of the Gram-negative coccus type, further comprising subjecting said sample to treatment with a lysis buffer comprising lysozyme. Also, when said Gram-staining indicates the presence of a Gram-positive bacterium in said sample, said method is further comprising determining the rod or coccus character of said bacterium, and when said Gram-positive character is of the rod type, further comprising subjecting said sample to treatment with a lysis buffer comprising lysozyme and/or Proteinase K.

[0025] In addition, when said character is of the Gram-positive coccus type, a method is provided further comprising determining a chain-like or clump-like character of said bacteria before a hybridisation protocol is selected. When before mentioned character is chainlike, a method provided by the invention is further comprising subjecting said sample to treatment with a lysis buffer comprising lysozyme, and further comprising hybridising said sample with at least one probe selected from a group of probes capable of hybridising with nucleic acid found in *Enterococcus faecalis*, in *Streptococcus pneumoniae*, in *Streptococcus mitis*, in *Streptococcus viridans*, in *Streptococcus sanguis*, in *Enterococcus faecium*.

[0026] In addition, a method is provided wherein said character is clump-like, further comprising subjecting said sample to treatment with a lysis buffer comprising lysostaphin and or Proteinase K, further comprising hybridising said sample with at least one probe selected from a group of probes capable of hybridising with nucleic acid found in *Staphylococcus aureus*, in *Staphylococcus haemolyticus*, in *Staphylococcus saprophyticus*.

[0027] Probes used in a method as provided by the invention can be directed against various target nucleic acid molecules found in a bacterium which can be used are for example ribosomal RNA, mitochondrial RNA, plasmid DNA, messenger RNA and nuclear DNA. It is also possible to select as target molecules nucleic acid from the above discussed antibiotics resistance genes, which can be found in a plasmid or integrated in the bacterial genome.

[0028] In a preferred embodiment, a method provided by the invention uses as a target for *in situ* hybridisation a (16S) ribosomal RNA molecule. In a particular embodiment of the invention said probe is having no more than five, preferably no more than two mismatches with a probe selected of a group composed of probes having a sequence GCCTGCCAGTTTCGAATG or GTAGCCCTACTCGTAAGG or GAGCAAAGGTATTAACCTTTACTCCC or GTTAGCCGTCCTTTCTGG or TTATCCCCCTCTGATGGG or AGAGAAGCAAGCTTCTCGTCCG or GCCACTCCTCTTTTCCGG or GCTAATGCAGCGCGGATCC or CCGAAGGGGAAGGCTCTA or AGAGAAGCAAGCTTCTCGTCCGTT, each selected in relation to a method as provided by the invention or in relation to congruent antibiotic sensitivity of a bacterium recognised by said probe.

[0029] In addition, a method is provided by the invention that is further comprising hybridising said sample with at least one positive control probe capable of hybridising with nucleic acid found in a majority of bacterial species and/or with at least one negative control probe not being capable of hybridising with nucleic acid found in a majority of bacterial species. Preferably said majority comprises at least 90% of bacterial species, especially with those species found in general with possibly infected (septicaemic) patients. A method as provided by the invention is even more specific and/or sensitive when at least 95%, preferably at least 99% of said species is reactive with said positive control probe or no more than 5%, preferably no more than 1% is reactive with said negative control probe.

[0030] Such a positive or negative control probe as provided by the invention is given in the experimental part, in general said positive control probe comprises no more than five mismatches with a probe with the sequence GCTGCCTCCGTAGGAGT and/or said negative control probe comprises no more than five mismatches with a probe with the sequence ACTCCTACGGGAGGCAGC.

[0031] Furthermore, the invention provides a method with additional value to the clinician in that in said method a probe is selected for its reactivity with one or a group of bacterial genera and/or (sub)species having congruent susceptibility to antibiotic treatment. Such a probe detecting or identifying a bacterium in a sample, preferably a clinical sample, is capable of hybridising with nucleic acid found in a group of bacterial genera and/or species or subspecies such as found with *Staphylococcus* and many other bacteria having congruent susceptibility to antibiotic treatment.

[0032] In a preferred embodiment of the invention, such a probe is having no more than five, preferably no more than two mismatches with a probe selected of a group composed of probes having a sequence GCCTGCCAGTTTCGAATG or GAGCAAAGGTATTAACCTTTACTCCC (i.e. reactive with bacteria for which amoxycillin treatment is most likely effective) or GTAGCCCTACTCGTAAGG (cephalosporin treatment) or GTTAGCCGTCCTTTCTGG (piperacillin and/or aminoglycoside) or TTATCCCCCTCTGATGGG or GCCACTCCTCTTTTCCGG (amoxycillin) or GCTAATGCAGCGCGGATCC or CCGAAGGGGAAGGCTCTA (vancomycin) or AGAGAAGCAAGCTTCTCGTCCGTT or AGAGAAGCAAGCTTCTCGTCCG (flucloxacillin).

[0033] In a much preferred embodiment of the invention a one-step procedure is used for both binding target bacteria (in the sample) to a microscopic slide and fixing intracellular structures. In the experimental part, various lysis buffers and fixating technique are provided that utilise such a one-step procedure.

[0034] Furthermore, the invention provides a diagnostic test kit comprising means for detecting or identifying a bacterium suspected of being present in a sample using a method according to the invention or using a probe according to the invention. Such a diagnostic kit for example at least comprises probes or a set of probes specific for the detection

of pathogenic bacteria. Instructions for a method comprising *in situ* hybridisation may be added. Optionally, said probes, which can be common nucleic acid or peptide nucleic acid probes, are linked to reporter molecules such as direct fluorescent labels. Other reporter molecules, such as enzymes or radioactive labels are also known.

[0035] In addition, said kit may comprise one or more of the necessary buffer solutions, such as lysis buffer or hybridisation, optionally in ready made form, or for example cover slips and reaction vials. Said kit may fully comprise sets of probes reactive with a wide gamut of (pathogenic) bacteria, optionally characterised by reactivity with bacteria of congruent antibiotic susceptibility, or may comprise sets of probes specifically directed against bacteria of Gram-positive or -negative, rod, coccus or chain- or clump-like character.

[0036] Such a kit may also comprise probes specifically reactive with antibiotic resistance genes, providing a positive identification of least applicable antibiotic treatment.

[0037] The invention is further explained in the experimental part of the description which is not limiting the invention.

Experimental part

[0038] An example of a set of probes specific for the detection of pathogenic bacteria and an example of a new protocol for high-speed *in situ* hybridisation are presented. The methodology described here is for example used for both a preliminary screening of samples from septicemic patients or as a full substitute on the basis of which therapeutic decisions are made. The invention thus provides a rapid and reliable method for determining the species and/or the genus of a bacterium present in a blood sample collected from a septicemic patient.

Components

[0039] A set of fluorescently labeled oligonucleotide probes designed to hybridise specifically with a group of pathogenic bacteria (i.e. *genus*-specific probe) or with one specific pathogen (i.e. *species*-specific probe) or with bacteria with congruent susceptibility or resistance to antibiotics.

[0040] A protocol for fast *in situ* hybridization of bacteria present in samples of blood collected from septicemic patients, using the said probes.

Oligonucleotide probes designed to hybridize specifically with a group of pathogenic bacteria.

[0041] In a particular embodiment of the invention a method provided by the invention is exemplified by making use of 16S rRNA target molecule because a large databank containing 16S rRNA-sequences exists and is freely accessible via the Internet. Labeled probes form an essential part in *in situ* hybridizations. The present invention provides a set of probes which have been designed in an unexpected novel manner i.e. not based on normal taxonomic principles but rather on their pathological significance. The group of probes which apply to this particular embodiment of the invention have been designed in such a way that they span group(s) of bacteria which are clustered on the basis of presumed congruent sensitivity to antimicrobial agents. Positive identification thus yields direct therapeutic information. Grouping bacteria on the basis of their presumed antibiotic susceptibility results in groups of bacteria containing one to several hundreds of different species. Although traditional methods can be used to detect the same set(s) of bacteria, the use of a set of probes based on the criteria of presumed antibiotic susceptibility patterns is much faster over classical culturing methods that still suffer from phenotypic variability induced by environmental factors. The probes are preferably labelled with enzymatic or fluorescent labels. Current fluorescent labels which are applicable in this invention are:

1) Direct fluorescent labels:

- Fluorescein-isothiocyanate (FITC)
- Tetramethylrhodamine-5-isothiocyanate (TRITC)
- Texasred™
- 5(6)-carboxyfluorescein-N-hydroxysuccinimide-ester (FLUOS™)
- 7-amino-4-methylcoumarin-3-acetic acid (AMCA™)
- Phycoerythrin
- Indocarbocyanine dyes such as Cy3™, Cy5™ and C7™
- Any other direct fluorescent label

2) Indirect fluorescent labels:

- Enzymes such as alkaline phosphatase or horseradishperoxidase either attached directly or via a C6-thiol linker and used in combination with chemiluminescent substrates like AMPPD (3-(4-spiroadmantane)-4-meth-

oxy-4-(3'-phosphoryloxy)-phenyl-1,2-dioxethane) or fluorescence generating substrates.

- Digoxigenin (DIG) in combination with anti-DIG antibodies labeled with:

- gold particles
- fluorescent labels
- Enzymes such as alkaline phosphatase or horseradish peroxidase, optionally in combination with chemiluminescent substrates like AMPPD (3-(4-methoxy-4-(3'-phosphoryloxy)-phenyl-1,2-dioxethane) or fluorescence generating substrates.

- Biotin in combination with streptavidin or avidin and labeled just like the anti-DIG antibodies
- Dinitrophenyl as hapten in combination with appropriate antibodies and labeled just like the anti-DIG antibodies
- Any other indirect fluorescent or enzymatic label

[0042] Fluorescent labels allow direct microscopic analysis preferably combined with image analysis. For the detection of fluorescent oligonucleotide probes hybridised to ribosomal RNA of the target bacterium, photography can be applied. However quantitation by this method is hampered by the absence of objective criteria by means of which discrimination between hybridized and non-hybridized cells can be performed. Therefore for objective evaluation of probe-specificity, an image analysis system is employed which allows fluorimetric reading of individual bacterial cells.

[0043] A protocol for fast *in situ* hybridization of bacteria present in samples of blood

[0044] Protocols for the detection of rRNA *in situ* typically utilise both a lytic reagent for permeabilisation of the bacterial cell wall and fixatives to preserve structural and molecular integrity of cellular components. However, the results of such hybridizations are highly dependent on the type, concentration and incubation-time of both the lytic reagent and the fixative. Component 2 of the invention consists of a protocol for *in situ* hybridization in which both permeabilization and fixation have been optimized for a subsequent hybridization of maximally 2 hours. For this protocol it was important to ensure that the hybridization procedure used was applicable to a wide variety of unidentified bacteria. Differentiated use of lytic reagents could only be based on information obtained from direct Gram-staining of the (pre-cultured) blood sample. After extensive validation the novel protocol had the following unique characteristics:

[0045] A optimal lytic reagent can be chosen on the basis of the gram-stain of the pathogen present in the sample of blood. This procedure of differentiated permeabilisation is novel to regular protocols for *in situ* hybridisation in which the permeabilisation is always dedicated to the permeabilisation of one or a defined group of target bacteria. In this new procedure a very wide array of unidentified bacteria can sufficiently be permeabilised without destruction of intracellular structures.

[0046] A one-step procedure is used for both binding target bacteria (in the sample) to the microscopic slide and fixing intracellular structures. Procedures presented in the current scientific literature all use multi-step protocols for binding, fixing and dehydration of the bacterial cells in order to condition them for optimal hybridisation.

[0047] The hybridisation time is shortened to 2 hours. Regular protocols for *in situ* hybridisation utilise a hybridisation time of minimally 24 hours, rendering them useless for rapid diagnostic applications.

[0048] The invention also provides kits for carrying out the rapid detection of bacteria in blood samples according to the invention. Such a kit will usually comprise at least a probe or probes and optionally other reagents such as components for hybridisation-fluid, washing-fluid and permeabilisation-fluid.

[0049] Such a kit may be applied in a routine bacteriology laboratory or in a bedside environment, both as a fast screening method or as a full substitute for classical identification methods.

Examples of probe design and development

[0050] The following probes for example were found to hybridise the most predominant species of pathogens which are found in blood from septicemic patients. In addition each probe hybridises with a species or a cluster of bacteria which share congruent (but often not identical) antibiotic sensitivity patterns

ID	Sequence (5'-3') ¹	Region ²	Specificity ³
5	A GCTGCCTCCCGTAGGAGT	V2	Bacterial Kindom
	B ACTCCTACGGGAGGCAGC	n.d.	no matches
	C GCCTGCCAGTTTCGAATG	V2	Salmonella spp, Klebsiella spp, Enterobacter spp.
10	D GTAGCCCTACTCGTAAGG	V7	K. oxytoca, S. marcescens, Enterobacter spp, Proteus spp
	E GAGCAAAGGTATTAACCTTACTCCC	V3	E. coli
	F TTATCCCCCTCTGATGGG	V2	E. faecalis
	G GCTAATGCAGCGCGGATCC	V2	S. aureus, S. haemolyticus
15	H CCGAAGGGGAAGGCTCTA	V6	S. aureus, S. saprophyticus
	I AGAGAAGCAAGCTTCTCGTCCG	V1	Streptococcus spp.
	J GTTAGCCGTCCCTTTCTGG	V3	P. aeruginosa
20	K AGAGAAGCAAGCTTCTCGTCCGTT	V2	S.aureus
	L GCCACTCCTCTTTTCCGG	??	Enterococcus faecium

¹ Each probe optionally contains an FITC-label at the 5'-end

² The variable region on the 16S rRNA where the target-sequence of the probe is positioned.

³ The species or genus which rRNA contains a match with the sequence of the probe.

Protocol example.

[0051] A newly devised protocol for fast in-situ hybridization of pathogens in blood from septicaemic patients. This version consists of a step-wise version which can directly be used in a laboratory environment.

1 Collect a sample of blood from a patient using a vacuum sealed culture bottle.

2 Place the culture bottle in the pre-culturing machine (e.g. BactAlert, Organon Teknika, Durham, NC 27704) to monitor the growth of the pathogen. On-line monitoring is performed by measuring the pH of the sample.

3 After bacterial growth in a sample of blood has been detected, perform a Gram-stain and take out the culture bottle and collect 1 ml. of blood from the bottle using a syringe.

4 Using the syringe, put +/- 0.1 ml of this sample on a degreased glass slide. And streak out using a slide of glass.

5 Dry the slide for 5 minutes on a hotplate (for example of approximately 50°C).

6 Fix during 5 min. in ethanol(96%):formaldehyde(37%) (9:1.)

7 Dry the slide for 5 minutes on a hotplate. (Slides can be stored for several months if kept at room temperature in a dry chamber)

8 Permeabilise **Streptococci** 20 min at 25 C with lysozyme (1 g/l)

9 Permeabilise **Staphylococci** 20 min at 25 C with Lysostaphin (100 units/ml)

10 Rinse the slide with (demineralised) water for 5 minutes

11 Dry the slide for 5 minutes on a hotplate.

12 Pipet hybridisation buffer(+SDS)-probe mix ([probe]=10ng/μl). Cover with a coverslip.

13 Hybridize 2 hours (for example at 48°C).

14 Rinse 5 min using hybridisation buffer(-SDS).

15 Mount the slide with a coverslip.

16 Evaluate the slide.

phosphate buffered saline

[0052]

- 8 g/l NaCl
- 0.2 g/l KCl
- 1.44 g/l Na₂HPO₄

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- 0.24 g/l KH_2PO_4
- adjust to pH 7.4.

Hybridisation buffer (+SDS)

5

[0053]

- 900 ml Milli-Q water
- 52.6 g NaCl
- 10 - 2.52 g Tris (hydroxymethyl)-aminomethane
- adjust to pH 7.5
- add 90 ml water.
- sterilize 15 minutes
- 10 ml SDS (10%) stock

15

hybridization buffer (-SDS)

[0054]

- 20 - 900 ml Milli-Q water
- 52,6 g NaCl
- 2,52 g Tris
- adjust to pH 7.5
- 100 ml Milli-Q water
- 25 - sterilize 15 minutes

hybridisation buffer-probe mix

[0055]

30

- 10 ng/ul of lyophilized probe in hybridisation buffer

lysozyme buffer

35 [0056]

- 1,2 g Tris (=100mM)
- 1,86 g EDTA (=50mM)
- add 100 ml of milli-Q
- 40 - adjust to pH 7.5
- 0,05 to 0,2 g lysozyme

Lysostaphin buffer

45 [0057]

- 1,2 g Tris (=100mM)
- 1,86 g EDTA (=50mM)
- add 100 ml of milli-Q
- 50 - adjust to pH 7.5
- 0,05 to 0,2 g lysostaphin
- dilute a lysostaphin stock (1000 ug/ml in milli-Q, stored at -20°C) 5-20 times in the above mentioned buffer.

[0058] Optionally, to lyozyme buffer or lyostaphin buffer 0,05 to 0,2 mg/ml Proteinase K is added.

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ethanol-formaldehyde (90:10)

[0059]

- 5 - 1 ml formaldehyde 37%
 - 9 ml ethanol 96%

Validation of probe specificity

- 10 [0060] Specificity of probes was tested against the complete RDA-database (<http://rdp-www.life.uiuc.edu:80/rdphome.html>) of 15 august 1996 using the CheckProbe command and was considered sufficient if a no more than five, preferably no more than two mismatches were observed. Furthermore, to determine whether the probes could reach their specific target sequence, a reference collection of 20 of the most predominant bacteria in sepsis were hybridised using both the protocol and the probes mentioned here above. The result of this validation is listed in table 2. As can be read from this table all probes yield a satisfying hybridisation profile. Using the group-probes C and
- 15 D it is possible to distinguish between: four groups of gram-negative rods:

- C-positive and D-positive: Klebsiella oxytoca, Enterobacter cloacae and Enterobacter aerogenes
 C-positive and D-negative: Klebsiella pneumoniae and Salmonella typhi
 20 C-negative and D-positive: Serratia marcescens and Proteus vulgaris
 C-negative and D-negative: Proteus mirabilis.

- For Escherichia coli and Pseudomonas aeruginosa two *species*-specific probes (E and J) have been designed and validated. These probes are optionally included because both Escherichia and Pseudomonas are notorious pathogens
- 25 which demand specific antimicrobial therapy. Probe F is a *species*-specific probe for Enterococcus faecalis, a notorious pathogen. Probe I is a *genus*-specific probe which can be used in conjunction with probe F because Streptococci and Enterococci share the same morphology, while they require different antimicrobial treatment. Using both probes G and H, 4 separate species of Staphylococci can be distinguished:

- 30 G-positive and H-positive: Staphylococcus aureus
 G-positive and H-negative: Staphylococcus haemolyticus
 G-negative and H-positive: Staphylococcus saprophyticus
 G-negative and H-negative: Staphylococcus epidermidis

- 35 Probe K is a *species*-specific-probe for Staphylococcus aureus and can be used to support the results obtained by probes G and H.

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Table 2.

Bacterium	A	B	C	D	E	F	G	H	I	J	K
<i>Escherichia coli</i>											
<i>Klebsiella pneumoniae</i>											
<i>Klebsiella oxytoca</i>											
<i>Serratia marcescens</i>											
<i>Enterobacter aerogenes</i>											
<i>Enterobacter cloacae</i>											
<i>Proteus vulgaris</i>											
<i>Proteus mirabilis</i>											
<i>Salmonella typhi</i>											
<i>Pseudomonas aeruginosa</i>											
<i>Enterococcus faecalis</i>											
<i>Enterococcus faecium</i>											
<i>Streptococcus pneumoniae</i>											
<i>Streptococcus mitis</i>											
<i>Streptococcus viridans</i>											
<i>Streptococcus sanguis</i>											
<i>Staphylococcus haemolyticus</i>											
<i>Staphylococcus aureus</i>											
<i>Staphylococcus epidermidis</i>											
<i>Staphylococcus saprophyticus</i>											

Legend: Probecoding see table 1, gray=positive hybridization, white=no hybridization

Testing a method in whole-blood samples.

[0061] Preliminary testing of a new method in 50 whole blood samples which were found positive upon pre-culturing yielded a correlation of 96% between a method described here and the classical culturing method which was also applied to each of the 50 samples.

However, the results of a method described here could be obtained within 3 hours while culturing results took a mean analysis-time of 32 hours.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

(A) NAME: Academisch Ziekenhuis Groningen
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(A) NAME: Rijksuniversiteit te Groningen
(B) STREET: Broerstraat 5
(C) CITY: Groningen
(D) STATE: Groningen
(E) COUNTRY: the Netherlands
(F) POSTAL CODE (ZIP): 9712 CP

(ii) TITLE OF INVENTION: Rapid bacterial determination.

(iii) NUMBER OF SEQUENCES: 12

(iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(v) CURRENT APPLICATION DATA:

APPLICATION NUMBER: EP 98201253.6

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GCCTGCCAGT TTCGAATG

18

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

GTAGCCCTAC TCGTAAGG

18

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GAGCAAAGGT ATTAAC TTTA CTCCC

25

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

GTTAGCCGTC CCTTTCTGG

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

TTATCCCCCT CTGATGGG

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

AGAGAAGCAA GCTTCTCGTC CG

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GCCACTCCTC TTTTCCGG

19

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

GCTAATGCAG CGCGGATCC

19

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

CCGAAGGGGA AGGCTCTA

18

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

AGAGAAGCAA GCTTCTCGTC CGTT

24

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GCTGCCTCCC GTAGGAGT

18

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

ACTCCTACGG GAGGCAGC

18

Claims

1. A method for determining a bacterium suspected of being present in a sample comprising
 - a) testing said sample by Gram-staining and
 - b) testing said sample with a probe according to an *in situ* hybridisation protocol selected on the basis of the outcome of said Gram-staining.
2. A method according to claim 1 wherein said sample is a clinical sample.
3. A method according to claim 2 wherein said sample is mammalian blood, preferably being derived from a human.
4. A method according to claim 1, 2 or 3 wherein said Gram-staining indicates the presence of a Gram-negative bacterium in said sample, further comprising determining the rod or coccus character of said bacterium.
5. A method according to claim 4 wherein said character is of the rod type, further comprising hybridising said sample with at least one probe selected from a group of probes capable of hybridising with nucleic acid found in *Escherichia coli*, in *Klebsiella pneumoniae*, in *Klebsiella oxytoca*, in *Serratia marcescens*, in *Enterobacter aerogenes*, in *Enterobacter cloacae*, in *Proteus vulgaris*, in *Proteus mirabilis*, in *Salmonella typhi*, in *Pseudomonas aeruginosa*.
6. A method according to claim 5 wherein said nucleic acid is ribosomal RNA.
7. A method according to claim 6 wherein said probe is having no more than five, preferably no more than two mismatches with a probe selected of a group composed of probes having a sequence GCCTGCCAGTTTCGAATG or GTAGCCCTACTCGTAAGG or GAGCAAAGGTATTAACCTTTACTCCC or GTTAGCCGTCCTTTCTGG.
8. A method according to claim 4 wherein said character is of the coccus type, further comprising subjecting said sample to treatment with a lysis buffer comprising lysozyme.
9. A method according to claim 1, 2 or 3 wherein said Gram-staining indicates the presence of a Gram-positive bacterium in said sample, further comprising determining the rod or coccus character of said bacterium.

10. A method according to claim 9 wherein said character is of the rod type, further comprising subjecting said sample to treatment with a lysis buffer comprising lysozyme and/or Proteinase K.
11. A method according to claim 9 wherein said character is of the coccus type, further comprising determining a chain-like or clump-like character of said bacteria.
12. A method according to claim 11 wherein said character is chain-like, further comprising subjecting said sample to treatment with a lysis buffer comprising lysozyme.
13. A method according to claim 12 further comprising hybridising said sample with at least one probe selected from a group of probes capable of hybridising with nucleic acid found in *Enterococcus faecalis*, in *Streptococcus pneumoniae*, in *Streptococcus mitis*, in *Streptococcus viridans*, in *Streptococcus sanguis*, in *Enterococcus faecium*.
14. A method according to claim 13 wherein said nucleic acid is ribosomal RNA.
15. A method according to claim 14 wherein said probe is having no more than five, preferably no more than two mismatches with a probe selected of a group composed of probes having a sequence TTATCCCCCTCTGATGGG or AGAGAAGCAAGCTTCTCGTCCG or GCCACTCCTCTTTTCCGG.
16. A method according to claim 11 wherein said character is clump-like, further comprising subjecting said sample to treatment with a lysis buffer comprising lysostaphin and/or Proteinase K.
17. A method according to claim 16 further comprising hybridising said sample with at least one probe selected from a group of probes capable of hybridising with nucleic acid found, in *Staphylococcus aureus*, in *Staphylococcus haemolyticus*, in *Staphylococcus saprophyticus*.
18. A method according to claim 17 wherein said nucleic acid is ribosomal RNA.
19. A method according to claim 18 wherein said probe is having no more than five, preferably no more than two mismatches with a probe selected of a group composed of probes having a sequence GCTAATGCAGCGCGGATCC or CCGAAGGGGAAGGCTCTA or AGAGAAGCAAGCTTCTCGTCCGT.
20. A method according to any of claims 4 to 19 further comprising hybridising said sample with at least one positive control probe and/or with at least one negative control probe.
21. A method according to claim 20 wherein said positive control probe comprises no more than five mismatches with a probe with the sequence GCTGCCTCCCGTAGGAGT and/or wherein said negative control probe comprises no more than five mismatches with a probe with the sequence ACTCCTACGGGAGGCAGC.
22. A method according to anyone of claims 1 to 21 further comprising a one-step procedure to bind bacteria present in said sample to a microscopic slide and simultaneously fix intracellular structures.
23. A method according to anyone of claims 1 to 22 wherein said probe is selected for its reactivity with one or a group of bacterial genera and/or species having congruent susceptibility to antibiotic treatment.
24. A probe detecting or identifying a bacterium in a sample, preferably a clinical sample, said probe capable of hybridising with nucleic acid found in a group of bacterial genera and/or (sub)species having congruent susceptibility to antibiotic treatment.
25. A probe according to claim 24 wherein said probe is having no more than five, preferably no more than two mismatches with a probe selected of a group composed of probes having a sequence GCCTGCCAGTTTGAATG or GTAGCCCTACTCGTAAGG or GAGCAAAGGTATTAACCTTTACTCCC or GTTAGCCGTCCCTTTCTGG or TTATC-CCCCTCTGATGGG or AGAGAAGCAAGCTTCTCGTCCG or GCCACTCCTCTTTTCCGG or GCTAATGCAGCGCGGATCC or CCGAAGGGGAAGGCTCTA or AGAGAAGCAAGCTTCTCGTCCGT.
26. A diagnostic test kit comprising means for detecting or identifying a bacterium suspected of being present in a sample using a method according to anyone of claims 1 to 23 or using a probe according to claim 24 or 25.



European Patent
Office

EUROPEAN SEARCH REPORT

Application Number
EP 98 20 1253

DOCUMENTS CONSIDERED TO BE RELEVANT			
Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	CLASSIFICATION OF THE APPLICATION (Int.Cl.6)
Y	EP 0 277 237 A (TORAY INDUSTRIES) 10 August 1988 * the whole document *	1-23	C12Q1/68 C12Q1/04
Y	WO 93 24659 A (MICROPROBE CORP) 9 December 1993 * page 2 - page 3; claim 1 *	1-23	
Y	FR 2 659 981 A (VEF SA) 27 September 1991 see abstract; claim 1	1-23	
Y	EP 0 479 117 A (HOFFMANN LA ROCHE) 8 April 1992 * the whole document *	1-23	
X	WO 97 05282 A (UNIV GRONINGEN ;WELLING GJALT WIETZE (NL); SCHUT FREDERIK (NL); LA) 13 February 1997	24,25	
Y	page 2 - page 3, ln 16; pages 12 and 13; claim 7.	1-23	
			TECHNICAL FIELDS SEARCHED (Int.Cl.6)
			C12Q
The present search report has been drawn up for all claims			
Place of search		Date of completion of the search	Examiner
THE HAGUE		10 November 1998	Osborne, H
CATEGORY OF CITED DOCUMENTS			
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